

Amendments to the Claims

This listing of claims will replace all prior versions, and listings, of claims in the application.

Listing of Claims:

1. – 9. (Cancelled).

10. (Currently amended) A method of inhibiting tumor growth in a mammal, comprising administering to said mammal a compound which inhibits expression of alpha-ketoglutarate-dependent dioxygenase aspartyl (asparaginyl) beta-hydroxylase (AAH), wherein said compound is a nucleic acid comprising an antisense sequence which is complementary to ~~a the 5' portion of the AAH regulatory sequence comprising~~ ~~cggaccgtgca~~ of SEQ ID NO:3, said antisense sequence consisting of 10 nucleotides in length and wherein said tumor overexpresses AAH compared to normal noncancerous cells.

11. – 12. (Cancelled).

13. (Original) The method of claim 10, wherein said tumor is derived from endodermal tissue.

14. (Original) The method of claim 10, wherein said tumor is selected from colon cancer, breast cancer, pancreatic cancer, liver cancer, and cancer of the bile ducts.

15. (Original) The method of claim 10, wherein said tumor is a CNS tumor.

16 – 38. (Cancelled).

39. (Previously Presented) The method of claim 10, wherein said tumor is a glioblastoma.

40. (Previously Presented) The method of claim 10, wherein said tumor is a neuroblastoma.

APPLICANTS: Wands et al.

SERIAL NUMBER: 09/436,184

41. (Previously Presented) The method of claim 10, wherein said tumor is a cholangiocarcinoma.
42. (Previously Presented) The method of claim 10, wherein said tumor is a hepatocellular carcinoma.
43. (Currently amended) A method of inhibiting tumor growth in a mammal, comprising administering to said mammal a nucleic acid, wherein said nucleic acid comprises an antisense sequence which is complementary to a 5' portion of ~~an~~ ~~the~~ AAH coding sequence of SEQ ID NO:3 and comprises a sequence complementary to the initiating ATG methionine-encoding codon of said SEQ ID NO:3, said antisense sequence consisting of between 10-50 nucleotides, inclusive, in length and wherein said tumor overexpresses AAH compared to normal noncancerous cells.
44. (Previously Presented) The method of claim 43, wherein said tumor is derived from endodermal tissue.
45. (Previously Presented) The method of claim 43, wherein said tumor is selected from the group consisting of colon cancer, breast cancer, pancreatic cancer, liver cancer, and cancer of the bile duct.
46. (Previously Presented) The method of claim 43, wherein said tumor is a CNS tumor.
47. (Previously Presented) The method of claim 43, wherein said tumor is a glioblastoma.
48. (Previously Presented) The method of claim 43, wherein said tumor is a neuroblastoma.
49. (Previously Presented) The method of claim 43, wherein said tumor is a cholangiocarcinoma.

50. (Previously Presented) The method of claim 43, wherein said tumor is a hepatocellular carcinoma.

51 – 71. (Cancelled).

72. (Currently amended) A method of inhibiting tumor growth in a mammal, comprising administering to said mammal a compound which inhibits expression of alpha-ketoglutarate-dependent dioxygenase aspartyl (asparaginyl) beta-hydroxylase (AAH), wherein said compound is a nucleic acid comprising an antisense sequence which is complementary to ~~a~~ the 5' AAH regulatory sequence cgaccgtgca of SEQ ID NO:3, wherein said tumor overexpresses AAH compared to a normal noncancerous cells, and wherein the length of said antisense sequence consists of between 10 – 20 nucleotides, inclusive.

73. (Previously Amended) The method of claim 43, wherein the length of said antisense sequence consists of between 10 – 20 nucleotides, inclusive.

74. (Currently amended) A method of inhibiting tumor growth in a mammal, comprising administering to said mammal a compound which inhibits expression of alpha-ketoglutarate-dependent dioxygenase aspartyl (asparaginyl) beta-hydroxylase (AAH), wherein said compound is a nucleic acid comprising ~~a~~ an antisense sequence which is complementary to ~~a~~ the 5' AAH regulatory sequence cgaccgtgca of SEQ ID NO:3, wherein said tumor overexpresses AAH compared to a normal noncancerous cells, wherein said antisense sequence consists of between 10-50 nucleotides in length, inclusive, and comprises a portion that is complementary to a 5' coding region of SEQ ID NO:3 which includes the ATG initiating methionine-encoding codon.

75. (Previously Presented) The method of claim 74, wherein said antisense sequence consists of between 10–20 nucleotides in length, inclusive.

APPLICANTS: Wands et al.

SERIAL NUMBER: 09/436,184

76. (Previously Presented) The method of claim 10 or claim 43, wherein said mammal is human.